

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2002, 22:11:20 ; Search time 17398.4 Seconds
(without alignments)
3374.551 Million cell updates/sec

Title: US-09-303-518d-651

Perfect score: 4350

Sequence: 1 atgaataacaccgacgaacg.....aattagctacgcgtgttaa 4350

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pin:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	1.4	839	12	CNS004NB
2	56.6	1.3	1101	12	CNS002Y3
3	55.4	1.3	1013	12	CNS016KT
4	55.4	1.3	1201	12	CNS016BA
5	52.8	1.2	914	12	CNS00CZP
6	52.8	1.2	925	12	CNS0091P
7	52.6	1.2	910	12	CNS006N
8	51	1.2	912	12	CNS006N3
9	50.2	1.2	1071	12	CNS00EM3
10	50	1.1	1101	12	CNS00EM3
11	49.2	1.1	1101	12	CNS017SY
12	48.4	1.1	838	10	CNS00BNG
13	48	1.1	852	12	B1949736
14	47.8	1.1	946	9	CNS011JX
15	47.6	1.1	1101	12	AI069309
16	47.4	1.1	932	12	CNS0016HG
17	47.2	1.1	955	12	CNS00E5F

C	18	47	1.1	1159	12	CNS015XR	AL106041 Drosophila
C	19	46.6	1.1	937	12	CNS006ST	AL065880 Drosophila
C	20	46.4	1.1	536	9	AN953567	AN953567 EST365637
C	21	46.4	1.1	605	9	BE060311	BE060311 HVM5E9001
C	22	46.4	1.1	1101	12	CNS0183L	AL108843 Drosophila
C	23	46.2	1.1	645	12	CNS01213	AL101589 Drosophila
C	24	46.2	1.1	815	12	CNS0200C	AL175845 Tetradon
C	25	46.2	1.1	919	12	CNS006S5	AL065856 Drosophila
C	26	45.8	1.1	1101	12	CNS012S8	AL101954 Drosophila
C	27	45.8	1.1	1129	12	CNS0020S	AL067824 Drosophila
C	28	45.6	1.0	1101	12	CNS002SC	AL067824 Drosophila
C	29	45.4	1.0	894	12	CNS01591	AL063305 Drosophila
C	30	45	1.0	1101	12	CNS01591	AL063305 Drosophila
C	31	44.8	1.0	1101	12	CNS00E5H	AL069702 Drosophila
C	32	44.6	1.0	1100	12	CNS016KD	AL106855 Drosophila
C	33	44.6	1.0	666	10	BC771741	BC771741 602720410
C	34	44.6	1.0	763	12	AF416119	AF416119 AF416119
C	35	44.6	1.0	949	12	CNS031R8	AL223901 Tetradon
C	36	44.6	1.0	1013	12	CNS016KT	AL106871 Drosophila
C	37	44.6	1.0	1101	12	CNS017RP	AL108415 Drosophila
C	38	44.4	1.0	1101	12	CNS0170B	AL108293 Drosophila
C	39	44.2	1.0	425	10	B1895704	B1895704 ERESTD23
C	40	44	1.0	462	9	AV435197	AV435197 AV435197
C	41	44	1.0	658	10	B1958152	B1958152 HVM5E9001
C	42	43.8	1.0	1101	12	CNS017YH	AL108659 Drosophila
C	43	43.8	1.0	474	9	BE050908	BE050908 za70h07.b
C	44	43.6	1.0	970	12	CNS010C9	AL098787 Drosophila
C	45	43.6	1.0	556	10	BE553144	BE553144 946089F12
C	46	43.4	1.0	504	10	C26583	C26583 C26583 Rice
C	47	43.4	1.0	1201	12	CNS016BQ	AL106544 Drosophila
C	48	43.2	1.0	450	9	AU181283	AU181283 AU181283
C	49	43.2	1.0	586	12	A2871772	A2871772 2M0145M17
C	50	43.2	1.0	675	9	AL507356	AL507356 AL507356
C	51	43.2	1.0	844	12	CNS012Z2	AL102233 Drosophila
C	52	43.2	1.0	953	12	CNS0052P	AL056652 Drosophila
C	53	43.2	1.0	1200	12	CNS017Y4	AL108646 Drosophila
C	54	42.8	1.0	609	10	BE266684	BE266684 601190221
C	55	42.8	1.0	711	10	BE264951	BE264951 601194055
C	56	42.8	1.0	826	10	BF626822	BF626822 HVM5E9000
C	57	42.8	1.0	1099	12	CNS03YCU	AL268151 Tetradon
C	58	42.8	1.0	1101	12	CNS00L72	AL068151 Drosophila
C	59	42.6	1.0	429	9	AW287177	AW287177 LGL1_267_P
C	60	42.6	1.0	906	12	AG082212	AG082212 Pan trogl
C	61	42.6	1.0	1038	12	CNS02YBW	AL219461 Tetradon
C	62	42.6	1.0	1101	12	CNS0181N	AL108773 Drosophila
C	63	42.4	1.0	315	12	CNS01677	AL106381 Drosophila
C	64	42.4	1.0	764	9	AL547921	AL547921 AL547921
C	65	42.4	1.0	890	12	CNS035KB	AL228836 Tetradon
C	66	42.4	1.0	918	10	B1760050	B1760050 603044519
C	67	42.4	1.0	1101	12	CNS017X5	AL108611 Drosophila
C	68	42.4	1.0	1679	10	BF698844	BF698844 602126407
C	69	42.2	1.0	816	12	CNS02BPN	AL190148 Tetradon
C	70	42.2	1.0	884	12	CNS00600	AL065923 Drosophila
C	71	42.2	1.0	910	12	AG032931	AG032931 Pan trogl
C	72	42.2	1.0	937	10	AI0895329	AI0895329 HS_4832_A
C	73	42.2	1.0	937	12	B1948506	B1948506 HVM5E1000
C	74	42.2	1.0	1055	12	CNS00BPU	AL069499 Drosophila
C	75	42.2	1.0	1758	12	AG063868	AG063868 Pan trogl
C	76	42	1.0	444	10	BM372986	BM372986 BMA04_50
C	77	42	1.0	922	12	CNS0073W	AL066784 Drosophila
C	78	42	1.0	1010	12	CNS016TE	AL107180 Drosophila
C	79	42	1.0	1019	12	CNS02HKM	AL197743 Tetradon
C	80	42	1.0	1101	12	CNS00LT2	AL078714 Drosophila
C	81	42	1.0	1101	12	CNS014Y2	AL104756 Drosophila
C	82	42	1.0	542	9	A1770803	A1770803 606058E10
C	83	41.8	1.0	689	10	BG859793	BG859793 1024065E0
C	84	41.8	1.0	866	10	B1951594	B1951594 HVM5E9000
C	85	41.8	1.0	917	12	CNS000CUT	AL059857 Drosophila
C	86	41.8	1.0	1031	10	BG777520	BG777520 602664869
C	87	41.8	1.0	1101	12	CNS00LXO	AL078875 Drosophila
C	88	41.8	1.0	1101	12	CNS00LXO	AL060137 Drosophila
C	89	41.8	1.0	1201	12	CNS00LXO	AL106054 Drosophila
C	90	41.8	1.0	1203	12	CNS015Y4	AL106054 Drosophila

[illegible]

RESULT 3
 CNS016KT/C-
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

CNS016KT 1013 bp DNA linear GSS 26-JUL-1999
 Drosophila melanogaster genome survey sequence SP6 end of BAC
 BACN16J16 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 AL106871
 AL106871.1 GI:5624218
 GSS.
 fruit fly.
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1013)
 Genoscope.
 Direct submission
 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr)
 Web : www.genoscope.cns.fr
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (EDGP) -
 http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
 library (Dros BAC) was made by Alain Billaud at CEPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBelobAC11.

FEATURES	
source	Location/Qualifiers
1..1013	
/organism="Drosophila melanogaster"	
/plasmid="pBel0BAC11"	
/db_xref="taxon:7227"	
/clone_11b="DrosBAC"	
/clone="BACN16J16"	
/note="end : Sp6"	
BASE COUNT	132 a 191 c 148 g 131 t 411 others
ORIGIN	
Query Match	1.3% Score 55.4; DB 12; Length 1013;
Best Local Similarity	26.3%; Pred. No. 0.014; Mismatches 109; Conservative 114; Indels 0; Gaps 0

[illegible][illegible]

CNS016BA/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CNS016BA 1201 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN15E04 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL106528
AL106528.1 GI:5622389
GSS.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1201)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
<http://www.edgp.ebi.ac.uk> -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaut at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pbeloRBAC11.

FEATURES	source	Location/Qualifiers
		1..1201
		/organism="Drosophila melanogaster"
		/plasmid="pBelobAC11"
		/db_xref="taxon:7227"
		/clone_lib="DrosBAC"
		/clone="BACN15E04"
		/note="end : SP6"
BASE COUNT	163 a	225 c 253 g 316 t 224 others
ORIGIN		
Query Match		1.3%: Score 55.4; DB 12; Length 1201;
Best Local Similarity		28.6%: Pred No. 0.015;
Matches 92; Conservative		87; Mismatches 143; Indels 0; Gaps 0

[illegible]

[illegible]

Db	698	SVSSSGTGTSTSSCGMSVCCSSSACVCWMSGCGCGCSCKCAGCCGCCSCCCACCAGCGGM	643
RESULT	6	CNS0091P	925 bp DNA linear GSS 03-JUN-1999
Locus	CNS0091P/c	Drosophila melanogaster genome survey sequence TET3 end of BAC #	
DEFINITION	BAC19916 of RPCL98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.		
ACCESSION	AL053013		
VERSION	AL053013.1	GI:4934461	
KEYWORDS	GSS.		
SOURCE	fruit fly.		
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
REFERENCE	Genoscope. 1 (bases 1 to 925)		
AUTHORS	Direct Submission		
TITLE	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr)		
JOURNAL	- Web : www.genoscope.cns.fr) Determination of this BAC end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and Est libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.		
FEATURES	source location/Qualifiers 1..925 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone_lib="RPCL98" /clone="BACR19D16" /note="end : TET3"		
BASE COUNT	120 a 61 c 61 g 172 t 511 others		
ORIGIN			
Query Match	1.2%, Score 52.8; DB 12; Length 925;		
Best Local Similarity	13.4%; Pred.No. 0.059;		
Matches	49; Conservative 163; Mismatches 153; Indels 0; Gaps 0;		
OY	3228 gccggcgcatgctccgcgcgaagaagcgttgcgaaccgccgcgngcagc	3297	
DB	918 SCSCSBBCSSMTSSNSBSBSSSCTSSBSSSSBSSSSGGTGTAA	859	
OY	3298 ggaggaaatgctgatattgcagcgaggaagaagaaaacgggttcagcggatcaa	3357	
DB	858 CVKCAASSCCGCGGMBACMCSSSSSCGSASAKGVKVRASGAGKRGGSAGASASH	799	
OY	3358 gacacgcntttggcgaacaacgcgaagcgaacccgcgcgnttaccaacgcctcc	3417	
DB	798 SSSSACBSSSSSCASCMASASSSSASSSRHSGGAGAGSGAASSRSSSSASAGSVY	739	
OY	3418 cgagcccgagcgcgcgcgcgcggatattgcgaacccgcgccccaacgcgaactcaccc	3477	
DB	738 SSASSSSSSSSSVSCSSVAASMGCSSSSSSSSSSSSSSSSACACCCCTTSMWSC	679	
OY	3478 caacgcgagcgcgcgcgcgcgcgcgttatgcgcgcgttatgcgcgttttgatgtaatlitcc	3537	
DB	678 STASMSARSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSGSGACGBSMSSCGG	619	

OY	3538	agccgaacaaggcttccgcgtacgaaccgattggaccgcgttttcgcgaagaccgc	3597
Db	618	SSSVASASGMSMSSVSSSGGRSGSGGGGGVGAGSSGSSSGGSGSVCSCSSQCMRC	559
OY	3598	cgcga 3602	
Db	558	SCSSA 554	
RESULT	7		
CNS0060N/c			
LOCUS			
DEFINITION	CNS0060N	910 bp	DNA linear GSS 03-JUN-1999
ACCESSION	Drosophila melanogaster genome survey sequence T7 end of BAC #		
VERSION	BACR14J21 of RPCT-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.		
KEYWORDS	AU065629		
SOURCE	AL065629.1 GI:4944698		
ORGANISM	GSS.		
AUTHORS	fruit fly.		
TITLE	Drosophila melanogaster		
JOURNAL	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
REFERENCE	1 (bases 1 to 910)		
COMMENT	Genoscope. Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org/The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm. Location/Qualifiers .1..910 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone_lid="RPCT-98" /clone="BACR14J21" /note="end : T7"		
FEATURES			
SOURCE			
BASE COUNT	202 a	63 c	112 g 198 t 335 others
ORIGIN			
Query Match	1.2%; Score 52.6; DB 12; Length 910;		
Best Local Similarity	17.6%; Pred. No. 0.066;		
Matches	59; Conservative 141; Mismatches 136; Indels	0;	Gaps 0;
OY	3171	cgcgaagcagaacccaaaaacagcgcggaagacagcgaacgcttcgacgcgc	3230
Db	836	SSVSIVSVSSASASAGTGRSASSVSIVSVSASRSRSASVSSSSSAGSAIVAVNAMCA	777
OY	3231	gatcgcgccggcgcatgctgcgcgcgaagaacgaagcgttcgaaaccgcgcggcn	3250
Db	776	SMVASVAVSVASVAVARAKSAKSAARAAVAAYARAKSAVAIVASASAIAVAIVASRV	717
OY	3291	ggcagcgcgggaaaaatgctcgcatltagcagcgcggaagagaagaacagcgtgcagc	3350
Db	716	ASASRRVMASGSSSSSSSSSSSSSSASAMVYSRGAVGVASASMAASARSASR	657
OY	3351	ggataaagcagcgcnttgcggaaacagcggaagcggaaaccgccgnttaccacgc	3410

[illegible]

[illegible][illegible]

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FEATURES
source
location/Qualifiers
1. 1101
   /organism="Drosophila melanogaster"
   /db_xref="takon:1227"
   /clone_lib="RPC1-98"
   /clone="BACR24B13"
   /note="end : TERT3"
BASE COUNT
129 a 276 c 132 g 151 t 413 others

```

Query Match	1.18;	Score 49.2;	DB 12;	Length 1101;
Best Local Similarity	22.18;	Pred. No. 0.5;		
Matches 78;	Conservative 109;	Mismatches 166;	Indels 0;	Gaps 0;

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 838)	Wing,R., Muehlbauer,G.J., Close,T.J., Kleinhofs,A., Wise,R., Heinemann,S., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,T., Fenton,R.D., Malatrasi,M., Choi,D.W., Oates,R. and Main	Development of a genetically and physically anchored EST resource for barley genomics: Fusarium infected Moxex spike cDNA library	Unpublished (2001)	Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu
Total hg bases	2453			
Seq primer:	AATTACCTCCTCAATAAGG			
High quality sequence stop:	570.			
Location/Qualifiers	1..838			

`/note="Vector: pBluescript SK(-); Site1: EcoRI; Site_2: XhoI;"`Plasmids were grown at the University of Minnesota at the GJ Muenbaur lab; spikes were harvested and snap frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium graminearum inoculation (Heinle). In the TJ Close lab at the University of California, Riverside, total RNA was

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Computerized (2000)
 Contact: John Quackenbush
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnq@tigr.org
 Plate: 52

JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequenca

Actinopterygii: Neopterygii: Teleostei: Euteleostei: Neoteleostei: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

source	<pre>1..1101 /organism="Drosophila melanogaster" /plasmid="pbelOBAC11" /db_xref="taxon:7227" /clone_lib="DrosBAC" /clone="BACN37J10" /note="end : SP6"</pre>
BASE COUNT	<pre>258 a 174 c 277 g 120 t 272 others</pre>
ORIGIN	
Query Match	<pre>1.0%; Score 44.6; DB 12; Length 1101; Best Local Similarity 28.7%; Pred. No. 6.9;</pre>
Matches	<pre>71; Conservative 65; Mismatches 111; Indels 0; Gaps 0;</pre>
Db 848	<pre>RAGAAARRAARARGRRRRAARAAGAARRRGAAGAARAARAGRMAARAARAARA 907</pre>
Qy 3205	<pre>aagaacaagacgttccgcacaactcggcaaggcagaaccgaataaacaggcgaaana 3204</pre>
Db 908	<pre>GAGARRARRARRGRRRRRAGARGGRGGRRRRRGGARRRGRRGHGARRAGG 967</pre>
Qy 3265	<pre>gaaacgcttgccgaaccgccgcngcagcgagcgagaaaatyltcgatcatltagcgcg 3324</pre>
Db 968	<pre>AGARRGRCGCCGCGRRRARARRRRGRRRGCGGAGAGGRCGGRAGGARAR 1027</pre>
Qy 3325	<pre>gaggaagagaaaaacgggtgcaggcggaataagaacagcgcntttgccaagcgcgaa 3384</pre>
Db 1028	<pre>RARRRRARRAGARAGARAGCGRRGRRGRRGRRGRRGRRGRRGRRGRRGRRGCGGAG 1087</pre>
Qy 3385	<pre>gcgga 3391</pre>
Db 1088	<pre>RRGGGRA 1094</pre>
RESULT 37	
LOCUS	<pre>CNS0170B 1101 bp DNA linear GSS 26-JUL-1999</pre>
DEFINITION	<pre>Drosophila melanogaster genome survey sequence SpE end of BAC BACN37H10 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.</pre>
ACCESSION	<pre>AL108293</pre>
VERSION	<pre>ALI08293.1 GI:5628597</pre>
KEYWORDS	<pre>GSS. fruit fly.</pre>
SOURCE	<pre>Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 1101)</pre>
REFERENCE	<pre>Title Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqret@genoscope.cns.fr Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CBPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pbeloBAC11.</pre>
COMMENT	
FEATURES	<pre>Location/Qualifiers 1..1101 /organism="Drosophila melanogaster" /plasmid="pbelOBAC11" /db_xref="taxon:7227" /clone_lib="DrosBAC" /clone="BACN37H10" /note="end : SP6"</pre>
BASE COUNT	<pre>238 a 262 c 313 g 51 t 237 others</pre>

ORIGIN	Query Match	1.0%	Score 44.4	DB 12	Length 1101
	Best Local Similarity	32.28	Pred. No. 7.7		
	Matches 140	Conservative	68	Mismatches 227	Indels 0
					Gaps 0
OY	3059	ccclucacaaacgaacacgctgatgcgagcgctgtgcgttacccaactcatccgcaagaagc	3118		
Db	585	CCGMAATYMRKMCACACACACCCSSRGCCGCCSVCGCGSGAATAAVGACCAACCAAAACMRA	644		
OY	3119	gcgaagttccgcctcgtcataatccggtcacaagaacaaagcttccgacaaactcggcaag	3178		
Db	645	CGMAAGCGCAAAARMFARCGGRARAAAAAGVAAAAAIVAAAGCGSSASRGCGAGGGAAGA	704		
OY	3179	cagaagcccaaaaaaagcgcgcaaaaaagcaacacgcgcgaagccttgaacgcgtcgtatgcg	3238		
Db	705	MGSMAAAAAAAGVGRSVSGAMSAAAAAAGVAAARCSAVAGGGGGAGAGCGCGAGGGGSGG	764		
OY	3239	ccgagcgcgatgcccgcgaaaaaagacagaagcgttgcgcgaacccgcgcgcgcgcgcgcgc	3298		
Db	765	GSAGCASSRGMAAAGSSCGGARAARCAARRAAAAAARGRCGGGGGGGSGSGSAGG	824		
OY	3299	gggaataatcgtcgcatatgtcaagcggaggaagaaaaaacgcggltgcagcgatgaag	3358		
Db	825	ARGGCGARGGGGSGSGSRGAGGCGSRRAAAAAAIAAAAAAAMCMGCGSGCCSG	884		
OY	3359	acagcgcnttggcgaacacagcgcggaagcggaacccgcgcgcgcgcgcgcgcgcgcgcgc	3418		
Db	885	RGGGMSGVSGSCGSGGCGCCCGSCGCGCCGCGCGSGGSGGCGSGAGCGCGCGSCCC	944		
OY	3419	gc	3478		
Db	945	SCGSCCCCCCCCCCGCGCCCGSCGSCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1004		
OY	3479	aaccgcgaagcgcgac	3493		
Db	1005	CCGSSCGCGSGSGVC	1019		
RESULT	38				
LOCUS	BI895704	425 bp	mRNA	linear	EST 15-OCT-2001
DEFINITION	ESTED2303.Y1 Eimeria tenella s5-2 cDNA Neg Selected Eimeria				
ACCESSION	BI895704				
VERSION	BI895704.1	GI:16138840			
KEYWORDS	EST.				
SOURCE	Eimeria tenella.				
ORGANISM	Eimeria tenella.				
REFERENCE	1 (bases 1 to 425)				
AUTHORS	Liberator,P., Diaz,C., Tang,K., Marra,M., Hillier,L., Kucaba,T.,				
	Martin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen				
	,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey				
	,N., Schurk,R., Ritzer,E., Kohn,S., Florence,N., Shin,T., Jackson				
	,Y., Cardenas,M., McCann,R., Watelston,R., Wilson,R. and Sibley,D.				
TITLE	WashU-Merck Eimeria tenella project				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: David Sibley, Ph.D.				
	WashU-Merck Eimeria tenella project				
	Washington University School of Medicine				
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA				
	Tel: 314 286 1800				
	Fax: 314 286 1810				
	Email: est@wustl.wustl.edu				
	Contact David Sibley (toxost@borcim.wustl.edu) for further				
	information relating to organism, libraries, or clone availability				
	Seq primer: -40RP from Gibdo				
	High quality sequence stop: 391.				
FEATURES	Location/Qualifiers				
SOURCE	1..425				

	source	1..474 /organism="Zea mays" /db_xref="taxon:4577" /clone="za70h07" /note="Vector: Lambda Zap II (Stratagene). Site: 1: XhoI; Site: 2: EcoRI; Resistance: Ampicillin/Auroxision: pBluescript SK (+/-) Titer: 7 x 10e-9 pfu/mL (as of 9/28/94)"
BASE COUNT	78 a 169 c 172 g 55 t	
ORIGIN		
Query Match	1.0%; Score 43.8; DB 9;	Length 474;
Best Local Similarity	45.9%;	Pred. No: 7.2; Indels 0; Gaps 0;
Matches 144;	Conservative 0; Mismatches 170;	Indels 0; Gaps 0;
OY 3647	cgcgaagtccgagcctaccgccacaacaaacggactcgccaataatcgatgcagaanaa	3706
Dd 325	GCGTGTACTCTCCTCCGTCGGAGACCACGCCGGCGGCCTTTGGCGGCTCTGCTCC	266
OY 3707	aacctggcaaggcgagcggtcgagcatcchytlttgcacaacggacggaananttcg	3766
Dd 265	CGCTCGAAGGCGAGCCCTCTCCTCGCGAGCGCGCACAGTGCGCCCTGAACCTTG	206
OY 3767	acgacggcatcggaactctgacagcggtcttgcccagcgcgcttttcggacataagca	3826
Dd 205	GGGGCGGAGCGGCAAGCGGAGCCCTTGCGCGGCGCCCTTGAGCGGCCACATGGC	146
OY 3827	tccgcaagttcgacttcgcatcacagagcgcggttttagcagcgganctntnca	3886
Dd 145	GAGCGGCGACACGCGGCCCCCTCTCTCGCGAGGCGCGGCTTCGACCTTGCAGGC	86
OY 3887	acggatcggaggaacaaatccgcgcgcgcytgtctgatcattgacattcagcataacc	3946
Dd 85	GCGGCTCGGCGCGCTTCGCGGCTTCCTCCGCCGCGCGCAGCGGGGACATTGGGG	26
OY 3947	gcgcgcggtttgcgc 3960	
Dd 25	CCCTCGGCTCGGCT 12	
RESULT 43		
CNS010C9/c		
LOCUS	CNS010C9 970 bp DNA linear GSS 26-JUL-1999	
DEFINITION	Drosophila melanogaster genome survey sequence SP6 end of BAC	
	BACN03L05 of DrosBAC library from Drosophila melanogaster [fruit	
	fly], genomic survey sequence.	
ACCESSION	AL098787	
VERSION	ALI098787.1 GI:5610398	
KEYWORDS	GSS.	
SOURCE	fruit fly. Drosophila melanogaster	
ORGANISM	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;	
	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	
REFERENCE	1 (bases 1 to 970)	
AUTHORS		
TITLE	Direct Submation	
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :	
	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr	
	- Web : www.genoscope.cns.fr)	
COMMENT	Determination of this BAC-end sequence was carried out as part of a	
	collaboration with the European Drosophila Genome Project (EDGP) -	
	http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC	
	library (Dros BAC) was made by Alain Billaud at CEPH (Centre	
	d'Etude du Polymorphisme Humain) with funding provided by a MRC	
	project grant. The DNA was prepared from embryos by Alain Bucheton	
	and Genevieve Payan. It has been constructed in the vector	
	peloBACL1.	
FEATURES	location/Qualifiers	
source	1..970 /organism="Drosophila melanogaster"	

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/plasmid="pbeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN03L05"
/note="end : SP6"

BASE COUNT      155 a       189 c       158 g       176 t       292 others
ORIGIN

Query Match             1.0% Score 43.8; DB 12; Length 970;
Best Local Similarity   20.0%; Pred. No.10;
Matches    51; Conservative 114; Mismatches    89; Indels    1; Gaps    1;

OY  3235 gcgcggcgagcgtatgccgccaagaacgaagcgttgcgaaccgcccgcgngca 3294
      |:: ::::|::: ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db   962 GASGASVVCSCMSAVAVRCASVYVCASASASCYCGSRSMVSVCSSVASRSSVAR-A 904

OY  3295 ggcggggaataatgttcgcatlatacgcaggcggaagaagaaaaagggltccagcgcat 3354
      ::::|::: ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db   903 VASVACARSRMSRAVARARVRCAGCASAAARSRYVVVRARAGVRAMARRRASAAVRVACA 844

OY  3355 aaagcacgaccttgccgaaaacgcgaaacgcgaaccgcgcgctgtaaccacgccttc 3414
      ::||::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db   843 RAGAARAARARGSVAVVGVRSVSVSSCSAAGRVMVCCCKGCRSASCVCAGMGSGSGC 784

OY  3415 cccgcgcgcgcgongccgcgcgcgcgatttgcgcgaaccgcagccccaacgcgaacctaa 3474
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db   783 SCMCASCSCCMCCCMCCAGSCCMCMGSCSGSCGSMVMSGCCCCCCTCVGMAGCGSM 724

OY  3475 ccccaaccgcagcgc 3489
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db   723 VMVCCCCCMRVSRM 709

RESULT  44
LOCUS    BE553144/c
DEFINITION  946089F12.y1 946 - tassell primordium prepared by Schmidt lab Zea
ACCESSION  BE553144
VERSION    BE553144
KEYWORDS   BE553144.1 GI:9794836
SOURCE     EST.
ORGANISM   Zea mays.
            Zea mays.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 556)
AUTHORS    Walbot,V.
TITLE      Walbot,V.
JOURNAL    Maize ESTs from various cDNA libraries sequenced at Stanford
COMMENT    University
            Unpublished (1999)
            Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 946089 row: F column: 12.
FEATURES
            Location/Qualifiers
                1..556
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                /cultivar="OH43"
                /db_xref="taxon:4577"
                /clone_lib="946 - tassell primordium prepared by Schmidt
                lab"
                /tissue_type="tassels"
                /dev_stage="just after the transition from vegetative to
                inflorescence development"
                /lab_host="XLDR"
                /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;
                Site_2: XhoI; George Chuck dissected immature tassels

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